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Comparative genomics of lupin rhizobial symbionts

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Native bradyrhizobial symbionts of lupins thriving in the Iberian Peninsula were studied. The analysis included five species that preferred neutral or acid soils: *L. angustifolius, L. luteus, L. hispanicus, L. micranthus* and *L. cosentinii,* and the unique, recently described lupin species *L. mariae-josephae*, endemic of alkaline Chromic Luvisol soils ("terra rossa") in Eastern Spain. Draft genome sequences of at least one strain from each lupin species were obtained by Illumina (PE, 2x300 bp, MySeq v. 3.0) sequencing, assembled with SPAdes, and annotated with the RAST server. Pairwise Average Nucleotide Identities (ANI) between genomes were calculated using JSpecies. The results showed a clear separation between strains nodulating *L. mariae-josephae* and those that nodulate lupins from acid soils. These results are in agreement with the observed host specificity, *i. e.* bradyrhizobia from *L. mariae-josephae* don't nodulate most of the lupins from acid soils and any bradyrhizobia from acid soil lupins do nodulate, although inefficiently, *L. mariae-josephae*. In contrast, acid soil lupins are efficiently nodulated by bradyrhizobia isolated from any of these lupins. Consistent with this, comparison of symbiotic regions (*nod*, *fix*, *nif* genes), showed maximum differences between *L. mariae-josephae* strains and those from other lupins. Another genomic features were also compared and results will be discussed.

Acknowledgements: Supported by MICINN (CGL2011-26932, to JI), by FBBVA (BIOCON08-078, to TRA), and by UPM (AL14-PI+D10, to LR), We thank A. Bautista and R. I. Prieto for technical assistance.